Cybergenetics

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REPORT
Cybergenetics: Boston
Lab: 13-07864, 13-08091, 13-08140

Victims: DONOHUE JR., Richard
COLLIER, Sean
MENG, Dun

Suspects: TSARNAEV, Dzhokhar
TSARNAEV, Tamerlan A.

Evidence Items:

Item 12-9.5.1	Swab/scrapings of interior palmar side of right glove recovered from driver side front floor area (Honda Civic MA Reg. 116GC7)
Item 12-1.1.1	KBS- Dzhokhar Tsarnaev
Item 15-1.1	KSS- Tamerlan A. Tsarnaev

METHODS:

- The DNA Identifiler® data profiles referenced in this report were previously developed and addressed in a DNA-STR Comprehensive Report issued by the Commonwealth of Massachusetts Department of State Police Forensic and Technology Center.
- The TrueAllele® Casework system processed each evidence item in independent replicate computer runs to infer possible DNA contributor genotypes from the samples.
- Some calculations assumed a reference genotype that involved comparisons to a different reference genotype.
- The DNA match statistics calculated herein used the population allele frequencies generated by the United States Federal Bureau of Investigation and a theta value (co-ancestry coefficient) of 1%.

RESULTS:

TrueAllele assumed that the evidence sample data (Item 12-9.5.1) contained three, four or five contributors, and objectively inferred evidence genotypes solely from these data. Following genotype inference, the computer then compared a genotype from this evidence item to provided reference (Items 12-1.1.1 and 15-1.1) genotypes, relative to reference populations, to compute likelihood ratio (LR) DNA match statistics. Based on these results:

A match between the glove (Item 12-9.5.1) and Dzhokhar Tsarnaev (Item 12-1.1.1) is:
2.98 million times more probable than a coincidental match to an unrelated Black person,
45.2 thousand times more probable than a coincidental match to an unrelated Caucasian person, and
24.1 thousand times more probable than a coincidental match to an unrelated Hispanic person.

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A match between the glove (Item 12-9.5.1) and Tamerlan A. Tsarnaev (Item 15-1.1) is:

9.84 million times more probable than a coincidental match to an unrelated Black person,
155 thousand times more probable than a coincidental match to an unrelated Caucasian person, and
70.6 thousand times more probable than a coincidental match to an unrelated Hispanic person.

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TrueAllele® Casework Method

Computer interpretation of DNA evidence

A definite genotype can be determined when a person's DNA produces unambiguous data. However, when the data signals are less definitive, or when there are multiple contributors to the evidence, uncertainty arises. This uncertainty is expressed in the resulting genotype, which may describe different genetic identity possibilities. Such genotype uncertainty may translate into reduced identification information when a comparison is made with a suspect.

The DNA identification task can thus be understood as a two-step process:

1. objectively *inferring genotypes* from evidence data, accounting for allele pair uncertainty using probability, and
2. subsequently *matching genotypes*, comparing evidence with a suspect relative to a population, to express the strength of association using probability.

The match strength is reported as a single number, the likelihood ratio (LR), which quantifies the change in identification information produced by having examined the DNA evidence.

The TrueAllele Casework system is a computer implementation of this two-step DNA identification inference approach. The computer objectively infers genotypes from DNA data through statistical modeling, without reference to a known comparison genotype. To preserve the identification information present in the data, the system represents genotype uncertainty using probability. These probabilistic genotypes are stored on a relational database. Subsequent comparison with suspects provides evidentiary identification information.

Many TrueAllele validation studies have been conducted to establish the reliability of the method [1]. Seven of these studies have been published in peer-reviewed scientific journals, on both synthetic [2, 3, 4, 5] and casework [6, 7, 8] data. Conducting such validations is consistent with the 2010 Scientific Working Group on DNA Analysis Methods (SWGDAM) interpretation guidelines [9] (paragraph 3.2.2).

References

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3. Ballantyne J, Hanson EK, Perlin MW. DNA mixture genotyping by probabilistic computer interpretation of binomially-sampled laser captured cell populations: Combining quantitative data for greater identification information. *Sci Justice.* 2013;53(2):103-114.
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5. Greenspoon SA, Schiermeier-Wood L, Jenkins BA. Establishing the limits of TrueAllele® Casework: a validation study. *J Forensic Sci. 2015:in press*.
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7. Perlin MW, Belrose JL, Duceman BW. New York State TrueAllele® Casework validation study. *J Forensic Sci.* 2013;58(6):1458-1466.
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9. SWGDAM. Interpretation guidelines for autosomal STR typing by forensic DNA testing laboratories. 2010; http://www.fbi.gov/about-us/lab/codis/swgdam-interpretation-guidelines